

C1  
9/2/12  
(1) GENERAL INFORMATION:

- (i) APPLICANT: He, Wei-Wu et al.
- (ii) TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
Like Apoptosis Protease 3 and 4
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Human Genome Sciences, Inc.  
(B) STREET: 9410 Key West Ave.  
(C) CITY: Rockville  
(D) STATE: MD  
(E) COUNTRY: USA  
(F) ZIP: 20850
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/462,969  
(B) FILING DATE: 05-JUN-1995  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/334,251  
(B) FILING DATE: 11-NOV-1994
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Brookes, A. Anders  
(B) REGISTRATION NUMBER: 36,373  
(C) REFERENCE/DOCKET NUMBER: PF140P1
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 301-309-8504  
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCACGAGAAA CTTTGCTGTG CGCGTCTCC CGCGCGCGGG CTCAACTTTG TAGAGCGAGG

60

GGCCAACTTG GCAGAGCGCG CGGCCAGCTT TGCAGAGAGC GCCCTCCAGG GACTATGCGT	120
GCGGGGACAC GGGTCGCTTT GGGCTCTTCC ACCCTGCGG AGCGCACTAC CCCGAGCCAG	180
GGGCGGTGCA AGCCCCGCCC GGCCCTACCC AGGGCGGCTC CTCCCTCCGC AGCGCCGAGA	240
CTTTTAGTTT CGCTTTCGCT AAAGGGGCCC CAGACCCTTG CTGCGGAGCG ACGGAGAGAG	300
ACTGTGCCAG TCCCAGCCGC CCTACCGCCG TGGGAACGAT GGCAGATGAT TCAGGGCTGT	360
ATTGAAGAGC AGGGGGTTGA GGATTCAGCA AATGAAGATT CAGTGGATGC TAAGCCAGAC	420
CGGTCCTCGT TTGTACCGTC CCTCTTCAGT AAGAAGAAGA AAAATGTCAC CATGCGATCC	480
ATCAAGACCA CCCGGGACCG AGTGCCTACA TATCAGTACA ACATGAATTT TGAAAAGCTG	540
GGCAAATGCA TCATAATAAA CAACAAGAAC TTTGATAAAG TGACAGGTAT GGGCGTTCTGA	600
AACGGAACAG ACAAAGATGC CGAGGCGCTC TTCAAGTGCT TCCGAAGCCT GGGTTTTGAC	660
GTGATTGTCT ATAATGACTG CTCTTGTGCC AAGATGCAAG ATCTGCTTAA AAAAGCTTCT	720
GAAGAGGACC ATACAAATGC CGCCTGCTTC GCCTGCATCC TCTTAAGCCA TGGAGAAGAA	780
AATGTAATTT ATGGGAAAGA TGGTGTCA CAATAAAGG ATTTGACAGC CCACTTTAGG	840
GGGGATAGAT GCAAAACCCT TTTAGAGAAA CCAAACTCT TCTTCATTCA GGCTTGCCGA	900
GGGACCGAGC TTGATGATGG CATCCAGGCC GACTCGGGGC CCATCAATGA CACAGATGCT	960
AATCCTCGAT ACAAGATCCC AGTGGAAGCT GACTTCCTCT TCGCCTATTC CACGGTTCCA	1020
GGCTATTACT CGTGAGGAG CCCAGGAAGA GGCTCCTGGT TTGTGCAAGC CCTCTGCTCC	1080
ATCCTGGAGG AGCACGGAAA AGACCTGGAA ATCATGCAAA TCCTCCACCA GGGTGAATGA	1140
CAGAGTTGCC AGGCACTTTG AGTCTCAGTC TGATGACCCA CACTTCCATG AGAAGAAGCA	1200
GATCCCCGTG GTGGTCTCCA TGCTCACCAA GGAACCTAC TTCAGTCAAT AGCCATATCA	1260
GGGGTACATT CTAGCTGAGA AGCAATGGGT CACTCATTA TGAATCACAT TTTTTATGC	1320
TCTTGAAATA TTCAGAAATT CTCCAGGATT TTAATTCAG GAAAATGTAT T	1371

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser

1	5	10	15
Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val	20	25	30
Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile	35	40	45
Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe	50	55	60
Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys	65	70	75
Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala	85	90	95
Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn	100	105	110
Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu	115	120	125
Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His	130	135	140
Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys	145	150	155
Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu	165	170	175
Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp	180	185	190
Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn	195	200	205
Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser	210	215	220
Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp	225	230	235
Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Glu Leu	245	250	255
Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His	260	265	270
Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile	275	280	285
Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln	290	295	300

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGCGG ATGGGTGCTA TTGTGAGGCG GTTGTAGAAG AGTTTCGTGA GTGCTCGCAG	60
CTCATACCTG TGGCTGTGTA TCCGTGGCCA CAGCTGGTTG GGGTCGCCTT GAAATCCCAG	120
GCCGTGAGGA GTTAGCGAGC CCTGCTCACA CTCGGCGCTC TGGTTTTTCGG TGGGTGTGCC	180
CTGCACCTGC CTCTCCCGC ATTCTCATTA ATAAAGGTAT CCATGGAGAA CACTGAAAAC	240
TCAGTGGATT CAAAATCCAT TAAAAATTTG GAACCAAGA TCATACATGG AAGCGAATCA	300
ATGGACTCTG GAATATCCCT GGACAACAGT TATAAATGG ATTATCCTGA GATGGGTTTA	360
TGTATAATAA TTAATAATAA GAATTTTCAT AAAAGCACTG GAATGACATC TCGGTCTGGT	420
ACAGATGTCG ATGCAGCAAA CCTCAGGGAA ACATTCAGAA ACTTGAAATA TGAAGTCAGG	480
AATAAAAATG ATCTTACACG TGAAGAAATT GTGGAATTGA TGCGTGATGT TTCTAAAGAA	540
GATCACAGCA AAAGGAGCAG TTTTGTGTTG GTGCTTCTGA GCCATGGTGA AGAAGGAATA	600
ATTTTTGGAA CAAATGGACC TGTGAGCTG AAAAAATAA CAAACTTTTT CAGAGGGGAT	660
CGTTGTAGAA GTCTAACTGG AAAACCCAAA CTTTTCATTA TTCAGGCCTG CCGTGGTACA	720
GAACTGGACT GTGGCATTGA GACAGACAGT GGTGTTGATG ATGACATGGC GTGTCATAAA	780
ATACCAGTGG AGGCCGACTT CTGTATGCA TACTCCACAG CACCTGGTTA TTATTCTTGG	840
CGAAATTCAA AGGATGGCTC GTGGTTCATC CAGTCGCTTT GTGCCATGCT GAAACAGTAT	900
GCCGACAAGC TTGAATTTAT GCACATTCTT ACCCGGGTTA ACCGAAAGGT GGCAACAGAA	960
TTGAGTCCT TTTCTTTGA CGCTACTTTT CATGCAAAGA AACAGATTCC ATGTATTGTT	1020
TCCATGCTCA CAAAAGAACT CTATTTTAT CACTAAAGAA ATGGTTGGTT GGTGGTTTTT	1080
TTAGTTTGT ATGCCAAGTG AGAAGATGGT ATATTGGGT ACTGTATTTC CCTCTCATTG	1140
GGGACCTACT CTCATGCTG	1159

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 277 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu  
1 5 10 15  
Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser  
20 25 30  
Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile  
35 40 45  
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg  
50 55 60  
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn  
65 70 75 80  
Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile  
85 90 95  
Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser  
100 105 110  
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe  
115 120 125  
Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg  
130 135 140  
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile  
145 150 155 160  
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser  
165 170 175  
Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp  
180 185 190  
Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn  
195 200 205  
Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys  
210 215 220  
Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn  
225 230 235 240  
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe  
245 250 255  
His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu  
260 265 270  
Leu Tyr Phe Tyr His  
275

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCGGATCC ATGCGTGCGG GGACACGGGT C

31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTACTCTAGA TCATTCACCC TGGTGGAGGA T

31

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCGGATCC ATGGAGAACA CTGAAAACTC A

31

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTACTCTAGA TTAGTGATAA AAATAGAGTT C

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTATGCGT GCGGGGACAC GG

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATCAAGCGT AGTCTGGGAC GTCGTATGGG TATTACCCT GGTGGAGGAT TTG

53

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCATGGAGA AACTGAAAA C

- 21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATCAAGCGT AGTCTGGGAC GTCGTATGGG TAGTGATAAA AATAGAGTTC TTT

53

*Conclude*